

22. (Reiterated) An isolated polypeptide selected from the group consisting of:

- a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-7,
- b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-7,
- c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-7, and
- d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-7.

23. (Reiterated) An isolated polypeptide of claim 22 comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-7.

31 24. (Once Amended) An isolated polynucleotide encoding a polypeptide selected from the group consisting of:

- a) a polypeptide comprising an amino acid sequence of SEQ ID NO:2, and
- b) a polypeptide comprising a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence of SEQ ID NO:2.

25. (Once Amended) An isolated polynucleotide encoding a polypeptide comprising an amino acid sequence of SEQ ID NO:2.

26. (Once Amended) An isolated polynucleotide of claim 25 comprising a polynucleotide sequence of SEQ ID NO:9.

27. (Once Amended) A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 24.

28. (Reiterated) A cell transformed with a recombinant polynucleotide of claim 27.

132 29. (Once Amended) A method of producing a polypeptide selected from the group consisting of a polypeptide comprising an amino acid sequence of SEQ ID NO:2 and a polypeptide comprising a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence of SEQ ID NO:2, the method comprising:

- a) culturing the cell of claim 28, and
- b) recovering the polypeptide so expressed.

30. (Once Amended) A method of claim 29, wherein the polypeptide comprises an amino acid sequence of SEQ ID NO:2.

31. (Once Amended) An isolated polynucleotide selected from the group consisting of:

- a) a polynucleotide comprising a polynucleotide sequence of SEQ ID NO:9,
- b) a polynucleotide comprising a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence of SEQ ID NO:9,
- c) a polynucleotide complementary to a polynucleotide of a),
- d) a polynucleotide complementary to a polynucleotide of b), and
- e) an RNA equivalent of a)-d).

33. (Reiterated) A method of detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 31, the method comprising:

- a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and

- b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

34. (Reiterated) A method of claim 33, wherein the probe comprises at least 60 contiguous nucleotides.

35. (Reiterated) A method of detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 31, the method comprising:

- a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and
- b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

36. (Reiterated) A method of screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence of claim 26, the method comprising:

- a) exposing a sample comprising the target polynucleotide to a compound, under conditions suitable for the expression of the target polynucleotide,
- b) detecting altered expression of the target polynucleotide, and
- c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

37. (Reiterated) A method of assessing toxicity of a test compound, the method comprising:

- a) treating a biological sample containing nucleic acids with the test compound,
- b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide of claim 31 under conditions whereby a specific hybridization complex is formed between said probe and a target

- polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 31 or fragment thereof,
- c) quantifying the amount of hybridization complex, and
 - d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

38. (Reiterated) A microarray wherein at least one element of the microarray is a polynucleotide of claim 32.

39. (Reiterated) A method of generating an expression profile of a sample which contains polynucleotides, the method comprising:

- a) labeling the polynucleotides of the sample,
- b) contacting the elements of the microarray of claim 38 with the labeled polynucleotides of the sample under conditions suitable for the formation of a hybridization complex, and
- c) quantifying the expression of the polynucleotides in the sample.

40. (Reiterated) An array comprising different nucleotide molecules affixed in distinct physical locations on a solid substrate, wherein at least one of said nucleotide molecules comprises a first oligonucleotide or polynucleotide sequence specifically hybridizable with at least 30 contiguous nucleotides of a target polynucleotide, and wherein said target polynucleotide is a polynucleotide of claim 31.

41. (Reiterated) An array of claim 40, wherein said first oligonucleotide or polynucleotide sequence is completely complementary to at least 30 contiguous nucleotides of said target polynucleotide.

42. (Reiterated) An array of claim 40, wherein said first oligonucleotide or polynucleotide sequence is completely complementary to at least 60 contiguous nucleotides of said target polynucleotide.